SEQUENCE LISTING

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SEQUENCE ID NO: 5, PCR primer

5'-TGGAAGCCAGAGACAAGCAG-3'

SEQUENCE ID NO: 6, PCR primer

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SEQUENCE ID NO: 7, PCR primer

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SEQUENCE ID NO: 8, PCR primer

5'-CTCAAACCACAGGCCTCCGGA-3'

SEQUENCE ID NO: 9, murine Socs2 locus

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KEYWORDS    .
SOURCE      house mouse.
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Mus.
REFERENCE   1  (bases 1 to 13908)
  AUTHORS   Horvat,S. and Medrano,J.F.
  TITLE     A 500-kb YAC and BAC contig encompassing the high-growth
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            in mouse chromosome 10 and identification of the murine
Raidd/Cradd
            gene in the candidate region
  JOURNAL   Genomics 54 (1), 159-164 (1998)
  MEDLINE   99026139
   PUBMED   9806843
REFERENCE   2  (bases 1 to 13908)
  AUTHORS   Horvat,S. and Medrano,J.F.
  TITLE     Lack of expression of Socs2 causes the high growth phenotype in
            mice
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 13908)
  AUTHORS   Wong,M.L. and Medrano,J.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-AUG-2000) Department of Animal Science,
University of
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8941 ttgggagtga ggaggcagtc agaagaccct gtgcctgtgg agttatgaca agctcccgag
9001 tgttgcgttc agcgcctgca ggtgtgtgtg tattgggagc ccagattcac tgcttggggc
9061 tgtgatatgg atcaccttat ctaactctag tcctgatggc aaggaagttg ataggcatca
9121 ggggacagtt ttgttttgtt tttgttttct tgctttatag tttttaatat atttactgag
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9181 ttccttgtgt gccagcctct gactcaatac ttcataatat ctcatttgat cctcggaagg
9241 accaaaagag caaagtccag gatttatggg aagtgaatag ttccacactg atccagttaa
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9481 cttctccgtt cttgcctctc gctgcgtggg ctccagggat tggacctcag tctttaccga
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9961 atcccatcta aagttaccaa cacagataac agatgtaatg acatctgctt tcttttaga
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10561 aacatacaaa cccagagctt aggtccggtg gaagctccac ccttctgccc tcccttcaaa
10621 ccgcctgtgc ccttctttgc tgcagttact gtaacttaaa acttgcttcc tctgacatgc
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10861 caagcatcct accgttgagc cacatctcca gtccatgtca atgtctctct aatctgtttg
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10981 agatgtcacc cacacatggc cagggtgccc agctgactct actctcctgt gtttgcttac
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11281 aaaccaaagc cagttcctaa caccacattt caacacttta aaaaaaaaaa aaaaaaaaaa
11341 acttgtttat ttaaacaacc gtaggctcct tacttgctag tttatgctct attgggaagg
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11641 tggtcttcct acccaccctg tcctcagctc tgtccacaag ggaggtctga gctgccaagt
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11761 agacaactct cactttgaac tccattcttc acttggagaa gaaggcgctg cccctcgagc
11821 aggagcagtt tgtgacgggt tatacagccc gtctgtggcc tcatctcagt gaggaacaga
11881 gggaagggag actcaagcca gagagagcct tggtgcgagc taagaaaata acaccagctg
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12121 ctttgggcag ccctttttct gttcagattt tgatcttgtg ttgctatgat ctttcttagt
12181 ctttcaggaa aacccctccc atgttgtttt ctgcccaggg aagttgtttt cccacttgga
12241 ctttcgtcac ccagatgaac tgatgaactg cgttccctta ggtagtagac ggaatcgtgg
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12421 ccgttcattc tcactggaac cactgtcaga aaaatggctt catgtcatta ttatttaagt
12481 atattgaagg cagtaatagg gttgggcaaa gaaaaagggg tgaagcctca ctggtgtgat
12541 gaggggctct tccgagtctc tcattaggta cccagggctc tcaagactat gaccagttta
12601 tttctatcac cctgtgtacc aatccttgct cttgagctgg ggtaggattg aacagcttta
12661 gcggaaaaaa aaattcttct tctaagacag ggccttaggt atcctagact cgaattggaa
12721 ctcgatgtag agctaagggt tatcctgaac tcctgaccct cctgcctccg tctttcagct
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12841 ttcctgggct ccaggcaagt tcttgaccaa gtgagctact ttcccggaaa ctggcaatca
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12961 gggcgctttc tgattcagca tcttttctc atccgttaca gtgttatctg tagagtttag
13021 agttgcagag aatggatatc cttcaagtct ttatttttt ttaatgatat attttatgta
13081 tgtgtgcatg taatgtgtat gtacacacac acacacacac acacacacac acacacacac
13141 acacattcat gtagatacc agaaaagacc agaagaagat gtcagattat ggttctgagc
13201 tgctatgtgg gagttgggaa ttgaattccg gtcctctgga agagcagtaa atgctcctgg
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13261 tgtcagagcc atctctcctg tccccatcca caagtcttgg gaccaaggcc taataaatca
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13381 gggaagagtc acactctcac attatagagg ccctcttacc ttatgggaag agatagagaa
13441 gacaggattc atatttattc aatagtctgg tctgtctcat gccccattgg ttaatctcca
13501 caacagccag gagcattaca gactcctttt attgaaaata aaacagatgc ttgaagatgg
13561 aaactgtagc gcccagcaat actgccctac gactaggagt ctgtacctgt atggagacta
13621 tggaacacac gcagggttat agctatgagt gacaccatgc tctcctctcc tcttagtctg
13681 ataaagcatt ccttacatga gagaactggc ttaggcttgt gctgtgtact gtccttctgg
13741 actccctggg tggtaggact tagaggtgaa gagtgagaga tgtgtggcgg gcaggcagga
13801 agcaggtgcc tgggagagga gtggagaggc agacaagatg ttcaagtttg tcaccgggct
13861 cagatttgtc ccagatttgt tccagattaa tttggagctc tgggtctg
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SEQUENCE ID NO: 10, exon 2 probe

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4501  AGTGTCTGCG AGAGACTTTG CCACACCATT CTGCCGGAAT TTGGAGAAAA AGAACCAGCC
4561  GCTTCCAGTC CCCTCCCCCT CCGCCACCAT TTCGGACACC CTGCACACTC TCGTTTTGGG
4621  GTACCCTGTG ACTTCCAGG
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SEQUENCE ID NO: 11, exon 3 probe

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6929  CTCGCCATTA ACAAATGTAC CGGTACGATC TGGGGACTGC CTTTACCAAC AAGACTAAAA
6989  GATTACTTGG AAGAATATAA ATTCCAGGTA TAAGTATTTC TCTCTCTTTT TCGTTTTTTT
7049  TTAAAAAAAA AAAAAACACA TGCCTCATAT AGACTATCTC CGAATGCAGC TAT
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SEQUENCE ID NO: 12, 3' Socs2 probe

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11185 GGAATTCAAG TCTACTTGAA TTAGGTAAAC TGACAGATTT AGGGTCCTTA GGATTAAGTC
11245 TGTGTCTGTT TCTCTTTAGT TCTCTTCAGG ATTTAAAAAC CAAAGCCAGT TCCTAACACC
11305 ACATTTCAAC ACTTTAAAAA AAAAAAAAAA AAAAAAACTT GTTTATTTAA ACAACCGTAG
11365 GCTCCTTACT TGCTAGTTTA TGCTCTATTG GGAAGGAAGA AAGACAGCCC TTCTTTAGCT
11425 TGTTTGTTGC TGAGGGCAAT CCTTGCACCT TCGGTTTGGT CTTCTCATTC TCTTCTGCTG
11485 CCCTGGAAGA TTTTCTCCAG TTTTCCCTCT ATGTGGTTTC AGAGTAAGTC ACCTTACCTC
11545 GCACTCAGCT TAAGGGACAG CTGTTGTTGG AGTCAGCCTC TAAAAGCCCC GTTTGTCCCA
11605 AATGCCTGAC TAGCGGGTCA GCTGAAGCAG TCATTGTGGT CTTCCTACCC ACCCTGTCCT
11665 CAGCTCTGTC CACAAGGGAG GTCTGAGCTG CCAAGTCTGA CGGGGGACTC ACTTCCATAA
11725 ACATTTACTG AGCCATAAAA ATAAAACTGC TTTTATAGAC AACTCTCACT TTGAACTCCA
11785 TTCTTCACTT GGAGAAGAAG GCGCTGCCC
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SEQUENCE ID NO: 13, HG deletion breakpoint 5' primer

5'-CTGGGCTCATTTTGGAAATG-3'

SEQUENCE ID NO: 14, HG deletion breakpoint 3' primer (I)

5'-TATTTTCTCCCAATAGCTCG-3'

SEQUENCE ID NO: 15, HG deletion breakpoint 3' primer (II)

5'-CTGGCTTCTGAAAACTTACC-3'

SEQUENCE ID NO: 16, HG deletion breakpoint 3' primer (III)

5'-GTAGATCTTGGGAGAGGAGA-3'

SEQUENCE ID NO: 17, HG deletion breakpoint 3' primer (IV)

5'-TGGGCTTTCCTTGGGAAAGTT-3'

SEQUENCE ID NO: 18, HG deletion breakpoint 3' primer (V)

5'-AGCTGTCGGCTGAAACGGAG-3'

SEQUENCE ID NO: 19, HG deletion breakpoint 3' primer (VI)

5'-AACGAAGTATCTTGAGTTAC-3'

SEQUENCE ID NO: 20, Merged Consensus genomic sequences of the high growth deletion in mouse chromosome 10.

The sequence covers a region of approximately 659,000 nucleotide bases of genomic DNA. Six BAC clones from the CITB mouse-BAC library corresponding to the minimal path of the physical map of the HG region (Horvat and Medrano, Genomics 54:159-164, 1998) were sequenced. The 6 BACs are: B520, B308, B546, B11I10, B9L14 and B405 and are assembled consecutively in 13 contigs. The contigs have been ordered and separated be sets of 20 Xs that identify gaps in the sequence.

The approximate location of the *hg* deletion is from nucleotide position 63,724 to 533,100. The breakpoint of the deletion in position 63,724 occurred in intron-2 of the mouse *Socs2/Cish2* gene (Accession # AF292933). The deletion of exon 3 of this gene eliminates the expression of this gene in hg mice and appears to be the causative reason of the high growth phenotype.

The deletion breakpoint at position 533,100 was determined because after this position is the sequence of the *Vespr* (viral encoded semaphorin receptor) gene (mRNA seq. Accession # AF190578), which is fully expressed in *hg*.

The deletion encompasses the full-length sequence of the RAIDD/CRADD gene (Accession # AJ224738) (from nt 146,837 to 298,188).

DEFINITION test, 659158 bases
ORIGIN

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      1  CTTGATGGAG TCGGTTGGGG TTTTTTGTTT GTTTGTTTGT TTGTTTTCTG
     51  GAAAGTTGAT AAACTTAATG AGGACATGGC TTGCAGCGTG GCAGGCACAA
    101  CACCTGATGC TAAGGTCCTG ACTAATTCAT TGCTCAGAGG TATTTATTCC
    151  AGTAACAGGA GCCAATTCCA CGTGCGCAGT TGTTTACAGC ACTGTGCTAT
    201  CACAGAGGCG CATGCGCAGT TTGGAGGGAA GTGTCCGGTT GCTGTTTCCT
    251  TGCTGTGTAT TGGCTGGGGT AAGCACCATG GCTTTCAGGT CTGTTAAGAG
    301  TGACCCAAGC GCATGAGCAT TGGAGACAGC AGTGCCCGAG CTGTGTCAGT
    351  GTTGAAACCA GACTACAACG CAGGAGAAAG GACTCTGAAG TCGACATTCG
    401  CTCTAGCTGT CAAGATGATA AAAAAATAAG ACAATAGATG TTGGTAAACT
    451  GTCAGCTGAA GAAGTAGAAA TGGCCACCCT AAGGAGAGAA TGGAATGGCC
    501  GTGAGCATGG TCCTCAGGCA AAGGAAGTGG AACAGTTGAC CAAAAACCAA
    551  GAAGAGGTAG AAGGGAAATC TCAGCAGGAG AAGGAGAGGG AATGGAAAGG
    601  AGAAATAGAC AAAATCGTGG ATTTTATAAC TCCCGAGAGG CACCAATTCT
    651  GTTAGAAGCC GTCCTGGCCT TTCACTCCGG AAAGGTTTTC TTGTTTTTTC
    701  TTTTTTAAGT TGCCCATCAG GGAATTAGGC CATTAATACT GAATCGGATC
    751  CTTGTCTGTC CAGTTGGGTG CTTTATTGTA ATGATGGACA TCTTTATAAA
    801  CATCTTAATC TTAATACATA ACTTTTTGGA ATAAAACTTA GACTGACAAA
    851  AACAGAATAG TGAACAAAAG AGAAGAAGGT TAGCAATAAT TGACAGTAAT
    901  GTGAACCTCT TGCCCAATGG GAGCACTTAG GTTCTCTCTC TTTTTTTTAT
    951  TGCATCAAAG AAAGTAAGTC TGATACAAGC TTGTCAGATA TACCAACTTT
   1001  GCTCCTAACT TTAAAACACT ATTAGTCTTT TTCAAATTTA TACCGAACAA
   1051  AGCTATTTAT TTGACGGACA AGTTGTATAT TGACTTATCT GAACAAGCTA
   1101  TTTCTATTGA AAAAAATTAT ATTGACTTAT AATAAAAGTT TTACAAGATC
   1151  AAGATAAGTT ATGAGCATGA AAGAACAAGG CTTGTAAGTA AAATTAAATA
   1201  ATTAAAAAGT GTTTCTGTGA GTCCAGAGTT GACCAATGTG GAACTCTAGA
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1251  AGGCCAAACG CAGTCCTGTG TGAGTACTTT AGCAAATTAG ACTTTAATGT
1301  ATTGAAAATA TAGATTAATG TAGTTCCTGA ATTATGTCTT TTTTTGTTTG
1351  TTTGTTTGTT TTTGTTTTTT TTTTTCGAGA CAGGGTTTCT CTGTGTAGCC
1401  CTGGCTATCC TGGAACTCAC TCTGTAGACC AGGTTGGCCT TGAACTCAGA
1451  AATCCGTCTG CCTCTGTCTC CTGTGTGCTG GGATTAAAGG CGTGCGCCAC
1501  CACGCCCGGC TCCGAATTAT GTCTTTCATG TGTTGCTGAT TTTGAGTTTT
1551  CTAAACAAAT AGTAACCCAT CACAGTCTTA CTTCCTCTGT ATCTTCCTAT
1601  CTCTTCCATG GCTGAGACAA AACTATTACC TTCCTCACTA CCCTTCTATG
1651  AAAAACCACT TACAGGTTTT AGTGGCCATT TACAATTACA TGTGAGGGAT
1701  GCTACTTTAA AAGCAGCCCT AGGAAGAGCC GGAGAGGCTG TGTTGCCTTA
1751  ACCTGCGGAA CACATTCTCG ACGAAACCGC CAGAGGGCAC TGTGACACAG
1801  CATTCAGCCT GAACCGCTTA CCCTGTGGTT GTGACTTTGA AATGCCAGAA
1851  TGGCAGAGAA TTTGAACATT GCTACTTGAG AAAGGGTGGT TTGATAATGT
1901  CATTGCCGGA AGTCGTTCTA CTCGTCTATC ATTAAGTATT TATACAACAG
1951  CTGGTTGTGA GAAGATCTGC TTTCTAGCTG GCCAACTCAA ACATCCTTAA
2001  GATCAGTGCT ACTTGCTAAA TATCGGCCGT GCTACTTATA TTTTTCTAAT
2051  GACATTCCCA ACTGTGGATG TTTTTCACTA TCATTTTTTT TAATTAAGTT
2101  TAGGTAGAAA ACCTTGACTT ACTCAAAGAT AACATTGTTA ACTGTTTTTG
2151  TACTTTCATA TATAAAAATA AATCTTTTAT GTATATTTAA AGACATCAGA
2201  TTTCTTTTTG TTAGAAAATA TGTTTTTTTT TAAAGATTTT TCTTTTAATG
2251  TGTATGGATG CTTTCGTTGC AGGTGTGTCT TAGTAACATG TGGGTGTCTG
2301  GTGCCCTTGT ATCTCCTGGG ACTGTAGTTA CAGACAGCTG GGAACTGACT
2351  GACATGTGGT GCTGGGAATT GAACTCAGGT CCCCTGGGAG AGCAGCCAGT
2401  GCTCTTGACT ACTGAGCCAT CTCTCCAGCC CTTGTACTTT CTTTTTGTTT
2451  TTAATTTTAA ATGGTGTGTG TTGTTTGTCT CTCGTCTCTC CACATGTGTC
2501  TGTCTGTGTA TATGTTGTCT GTCTGTCTGT CTCTCCGTGT GTGTGTGTGT
2551  GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT TCTGTTGGGG ACTGATCTCA
2601  GGGCTTTCTT TATACATGTC AGGCAAGCAC TGTGCCTCTG AATTGCCTCC
2651  TCACAAGGGC TAAGGGTTTT GTGACTCCTT CTTTTGGTCC CACAAACTCC
2701  TGCCTTCCTA AGAAGCTAAC AACTCTAGTC CCAGTCAGCA GAGGTAAGAG
2751  AACCCATTAG TTAAGACTCT TGATTTCCAG GGCCAAGAAG CCCATCCATC
2801  CACAGTAGAG TCCAGCAATG GGAGTCTGTT GGAGGAGGAT CACAGGACTG
2851  TAGGAAAGTG AAGCTGGACC ATGGGGAGAC GTCAGCTGAG GACTTGGTTC
2901  CTGCCAGTAG GCTTGCTTTT CATCTTTTGT GGTTGTTGTT GTTGTAAACA
2951  TTTATTCAAT GTATGAAGAG GGTGTTCAAT TCTCTCTTTC TACCACATGG
3001  GATCTGGATA TTGAACTTGG CCGGCTTGAC GGCAATCTCT TATACCTCCT
3051  GAAGTGTTTG GTAGTTCCCC GACTCCTGGT CTGTGTGTGT ATGTGTGTGT
3101  GTGTGTTCAT GCATACCCTG GTGTGGTGTG AAAGACAGAA GACAAACTTG
3151  GGGAGTTAAG TTTCAAGGCC TGAACTCAGG TCATCAGGCT TATACAGCAA
3201  GCACTTTTAC CCATCAACCA GTTGACGTGC CCATTGTTAA GCTGCTTGCC
3251  TCCTCCTCCT CCCCCTCCCC CTTCCTCCTC GTTTTCTTGT TGTTGTCGTC
3301  GTCATCGTCC TCGTTGTTTT TGAGATGAGG TCTCATAGCT CTAGCAGGCC
3351  TAGAACTTAC TGTGTAGGCC AGGCTGGCCT CTGTTTCCCG AGTGCTGAGT
3401  TTGAAGGCAT GTGCCACCAT GCAGGGCGGT TAGGCATCTT CTAGTGTGGT
3451  CATTTGATGA ATGTCTGTCT CTCCTACTAA GCTGTAACCT TCACAACTGG
3501  GATTGATGAC CTTATTAAGT TATGTGTCTT GCATGGCTCC TAGTGCTGGC
3551  ACTGCCTGGC CTTTTTACCA TCCCCACATA GTTTTGTAAA AGCAAACTGC
3601  CTTGGCATGA AGGATTTTAA GTAAGGAGTC CCTGTGGGAC TCAGGATAGA
3651  AATGTAGCCA CAGAACTCCT GAGACTGAAG GATTTTGAGA CAGTTTATTT
3701  GTGTGTTTTC TTGAACATAG AAACTGCAGT TTTAAAGCTG CTTATTAGAG
3751  TATTTTATAT CTCTCCTCAA CTTTACCTGC CTGCAGCTAA TCACTTAGTA
3801  ACATTAAAGC TGAAAAAATA TTCAAATACA AGACAGCTTC CATATGTTCT
3851  AGGAGACATC TTTATCTTTA ATTCCAACTA TATTTTTATT TGTGTGTGTG
3901  TTTGTGTGTG TATGTGTGTG TGTGTGTGTG TGTGTGTGTG TGTGTACATA
3951  GTTCCCATGG AAGTCAGAAG TGAGCACCAG ATTCCCTGGA GCTGCAGTGC
4001  CAGAAAGCAA GCCATGCAGG AGTTGAACTT GGGTTCTATG GAAGAGCAGC
4051  AGGTGCTCTT ACTGAGCAAT CTCTCCAACC CTAATTATAA ATACTTTTAA
4101  GAAAAGAGCT GGGCAGTGTT GACACAGGCC TTTAGTTCCA GCATTTGGGA
4151  GGGAGAGGCA GGTGGATCTC TTGAGTTCAA GGCCAGCCTG GTCTATAGAG
4201  CAAGCCCCAG GAAACAGAGA AACATTGTCT CAAAAACAAC CAACCAACCA
4251  AGAACAGCCA GCTTGCCAGC AGTTATTGCT TATGTTCTTC ATGAAAGCCA
4301  TTCTGACTTG GACCACATGA AATCACAATG TAGGAATATT TGTTTGTTTT
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4351  TGAGACAGGA TCTCTCATAG TGTCTGTCGG TCTCCACCCC CAAGTGCTGG
4401  GATGAAGGTG GGGGACCTTG GTCTGGCCCG TCTTCCCCAC CGAGCCGTGG
4451  GGGTGGAGCA TGAATATACA CATTGGGATG CTTCAGTGTA CTTTTTGATT
4501  TGCATTTTCT TGATGGTTAA GAATGCCAAA CATTTTTTCA TGTGTTTATT
4551  GCCCCCCCTT TAAAAATTTG ATCAGTATCT CTTTTGTTCA TCTGCCTACC
4601  AGTTGGTTGG ATTACTCATT CTTTTACTGT TCTTTATATA TTCTAGATAT
4651  TAGCTCCTTA TCAGATGAAT ACGATTCCTT TTTTCTTATT TTGTAGACTG
4701  TGGCTTTTTC TATTGATCGT TTTCTTTTGC TGCGTGGAGG CATTTTAATC
4751  TAGTGCCGTT TATCAGTTCT TCATCTTATT TCCTCTGCTA TTGGGGTCTC
4801  ATTGAGAGGG CCGGGCCGGT GAAATTGCTC AGCGGGTTAA GGCACTTACA
4851  GCTCAAACCT GGCAAACCAA CTGTGCTTCC CAGAACCCAC ATAGAGGTGG
4901  AAGGAGAGAA TCTATTCCAC GGAGAGAGCT ATTGTCTGCG CTGCTGTCTG
4951  CATGACCCTG TTTTCCCTCT AGTGATATAA ACTCTTATAA TACAAGTCTC
5001  TGTTCTTCAC TCCATTACTA GGCGGTCTTA TTATAAAGTG TTTACTTCCT
5051  TGGGATGAAA GCAGTGTTTC TATGGCTTGT AATTCTTACA CTTGATCCTA
5101  TCCCTAAAAT CACAAAATAA ATGGACTCCA TTTCACAGGC GACAGCTCTT
5151  TAGATACTCA AAAGCATTTG TCAGATCTCA TTATTATTCA CCCCCCCCCC
5201  ATTATCCGTA TGGCATGTTC TCCAAACCTC CCCAATTTTG GTTGCCCCTC
5251  CCCCTTTGAG CTATACATTC ATTCATCCTT TTAATAGCAT CTCTCTGAGA
5301  ATGTGTTACC CAGAACTGAG CGCAGTTTTC TTGCTCAGGA TGCTTTCATT
5351  GTGCTAATGG TGCCAGTAAC ACATTAAGGT TTTTAGTTTT TTTTGTTTTT
5401  TGTTTTTTTT AAGTAGTCGT GCCATCCAGC AGGTTCTCAC TGAGTCATAA
5451  TACCCTAAGA GGGGGTCAGA ATACCAAAAG AGGCTCTAAA TTTGGATGAT
5501  TTTTTAATGC AAATATACTT TCTGCTCTTC TTGATTCCTC GCTGGGAAGA
5551  GAGAACATTT ATTTGCATTG CTAACCGCAC TGGTTTTTAT TTTTGCCGTG
5601  TAATGTTAGC ACACAGCTGT CGATACCCAC CAAGGAAGAA TTTTAGCAGG
5651  GGATGACGCA TTTAGAAACC TCATTCTTGC TAAAGGGTGG ATAGGGAAGG
5701  ACAGATTGGA ATAGGAACAA GATGGAATGT CAGAGACACC ATTACGTGAC
5751  GTAGTGATGA GGATGACAGC TGACAATGGT TGGGGTTAGG AAAACAGCAG
5801  AAAGGATAGG AGGAGAGGCT GGATTTCAGA GAGACAGACA TAGTCATGTG
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5901  ATGAGACGGG GTGAGGCATA CACTCACACA CACAGTTACA CACTCACACA
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6051  TACACCCACT CACATACAAT ACAATCACAT ACACTCACAC AGTTACACAC
6101  TCACACACAC ACATACAATC ACATATACTC ACACACTTAC ACACTCATAT
6151  ATACTCACAC ACATCCATAC AATCACATAC ACTCACACAA GTTACACACT
6201  CATACACATA TTTACAATCA CATACACTCA CACACACAGT TACACACTCA
6251  TACATACTCA CACAAGTTAT ACAATCACAT ACATACAATC ACATACAATC
6301  ATATACACTC ACGCACAGTT ATACACTCAT ACAATCACAT AACTCACAGT
6351  CACATACATA CTCACATACC CCCATGCGCA CACACACACA CACACACACA
6401  CACACACACA CACACACACA CCACAGCTCT TGACATCCAG ATGACCCAGC
6451  TTTGGCAGTG AGGCCTGTGT TTTCCTGTTG GGTATATGAT CTTACAGCAT
6501  CTGGGCAATG TCCTTGGGGC CTGTATGAAA TGAGACACCC AATGTTCACT
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20601	AGTAGGTTTT	AAGGTCTTGA	GCCCTGTTAA	TACAGACAGT	GCGGCGGGAT
20651	GAGAGTGGTG	CCCATGGGCT	CCTGTGTTTC	GATGCTGCAT	TCCCAGTTAT
20701	GGAGCTTTGG	GGAAGGATTA	GGTTGGCTTT	GTTAGGGGAG	GTCTGTCATA
20751	AGGGGAGAGG	GAGGGACTTG	GAGGTTGCCT	GTTATATTAA	GAATTAATTA
20801	CCGGGCTGGA	GAGATGGCTC	AGCGGTTAAG	AGCACTGACT	GCTCTCTAGA
20851	AGGTCCTGAG	TTCAAATCCC	AGCAACCACA	TGGTGGCTCA	CAACCATCCA
20901	AAATGAGCTC	TGACGCCCTC	TTCTGGCATG	TCTGAAGACA	GCTACAGTGT
20951	ACTTACATAT	AATAAATAAA	TTAAAAAAAA	AAAAGAAAGA	AAGAAAACGC
21001	CGGGCGGTGG	TGGCGCATGC	CTTTAATCCC	AGCACTTGGG	AGGCAGAGGC
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21351	CAGCCCCATC	CCAGAATACT	TGCATATTAT	TATTGATCTT	CAGTCCTGTT
21401	CCTCATGGCT	CCAGTTCCTC	TGTTCTACCA	GTTCATCTGA	ATTTCCCTCT
21451	CTTCTCTTTT	TTCCTCTGGT	TGGCCAATGT	CCCACCCTCT	TCTCTATTCT
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22151	GCTGCAGACT	GTACCAAGCT	TGATACCAAC	TATACTTGTT	CTTCACTATC
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22301	ATTTCAGACT	TATGAATTGG	TTACTTCTAG	AATTTTCCAT	TTAATGTTTT
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22501	CAGTCTACCA	TAAAATATTG	TGTTAAATCC	AATGTTGGTG	AAGATAGTGT
22551	AATAATATAA	AAAAGATTCC	AGTGAAAAAC	ATATCTAGAA	AAGGGCCTGC
22601	GATTATAGAT	AAATATTTGC	CCTGTGAATA	CATGAATGCG	TATCACTTTA
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22701	TGTGAAGCCC	TGGCTGTCCT	GAAACTCACT	CTGTAGACCA	GGCTGGCCTC
22751	GAACTCAGAA	ATTCACCTGC	CTCTGCCTCC	CGAGTGCTGG	GATTAAAGGC
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22851	TTAAATGATC	TGGAGAGATT	ACATGGCCTC	ACCCTCAACC	CCTCCTCGGC
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